<u>REMARKS</u>

Claims 1-4, 7-12, 22, 31-33 and 35-39 were pending in the present application.

The Examiner states the proposed amendment to claim 4 submitted in a telephone interview on 06/10/2003 with Paul Paglierani has not been entered.

Applicants acknowledge the status of claim 4 and have made the amendments as recommended by the Examiner herein. Claim 35 has been cancelled, without prejudice, and claims 4, 12 and 22 have been amended. Support for the amendments made lie in the specification and original claims as filed. Any claim amendments should not be construed as acquiescence to any of the Examiner's rejections and were done solely to expedite prosecution of the application. No new matter has been added by virtue of the amendments.

Claim Objections

The Examiner objected to claim 12 because of the recitation of "culture medium to, thereby, produce the polypeptide." The Examiner suggested the use of the phrase "culture medium to produce the polypeptide."

In the interest of expediting prosecution, and without acquiescing to the Examiner's objection, Applicants have amended claim 12 as recommended by the Examiner, thereby rendering the objection moot. Applicants respectfully request reconsideration and withdrawal of the foregoing objection.

The Rejection of Claim 22 under 35 U.S.C. §112, Second Paragraph, Should Be Withdrawn

Claim 22 is rejected under 35 U.S.C. §112, second paragraph, as "being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention." Specifically, claim 22, which recites: "a kit comprising the nucleic acid molecule of any one of claims 1, 2, 3, or 4 which selectively hybridizes in 0.5M sodium phosphate, 7% SDS at 65°C, followed by one or more washes in 0.2 X SSC at 65°C, to a nucleic acid molecule and instructions for use" was rejected by the Examiner, who asserts that "the recited hybridization conditions are redundant since the kit already comprises the nucleic acid molecules of any one of claims 1, 2, 3 or 4." The Examiner suggests that the claim be amended to recite, "a kit comprising the nucleic acid molecule of any one of claims 1, 2, 3, or 4 and instructions for use."

In the interest of expediting prosecution, and without acquiescing to the Examiner's rejection, Applicants have amended claim 22 as recommended by the Examiner. Applicants respectfully request reconsideration and withdrawal of the foregoing 35 U.S.C. 112, second paragraph rejection over claim 22.

The Rejection of Claims 4, 7-12, 22, 31, 35-39 under 35 U.S.C. §112, First Paragraph, Should Be Withdrawn

Claims 4, 7-12, 22, 31, 35-39 are rejected under 35 U.S.C §112, first paragraph, as failing to comply with the written description requirement, since "the claims contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention." Specifically, the Examiner asserts that claims 4, 7-10, 22 and 35-39 are "directed to a genus of structural homologs of the polynucleotide of SEQ ID NO:1 of any function encoding a naturally-occurring variant of a polypeptide having kinase activity" and that "the specification only discloses a single species of the claimed genera." However, the Examiner notes "that the proposed amendment of claim 4 submitted by Applicants on 6/10/2003 appears to overcome the instant rejection."

In the interest of expediting prosecution, and without acquiescing to the Examiner's rejection, Applicants have amended claim 4 as recommended by the Examiner. Applicants respectfully request reconsideration and withdrawal of the foregoing 35 U.S.C 112, first paragraph rejection over claims 4, 7-12, 22, 31 and 35-39.

The Rejection of Claims 4, 7-12, 22, 31, 35-39 under 35 U.S.C. §112, First Paragraph, Should Be Withdrawn

Claims 4, 7-12, 22, 31, 35-39 are rejected under 35 U.S.C §112, first paragraph, "because the specification, while being enabling for the polynucleotide of SEQ ID NO:1, does not reasonably provide enablement for a structural homolog of the polynucleotide of SEQ ID NO:1, wherein said homolog encodes a polypeptide of any function." Specifically, the Examiner asserts that claims 4, 7-10, 22 and 35-39 are "directed to structural homologs of the polynucleotide of SEQ ID NO:1 of any function encoding a naturally-occurring variant of a polypeptide having kinase activity" and that the "scope of the claims is not commensurate with the enablement provided in regard to the large number of polynucleotides of unknown function encompassed by the claims." However, the Examiner notes "that the proposed amendment of claim 4 submitted by Applicants on 6/10/2003 appears to overcome the instant rejection."

In the interest of expediting prosecution, and without acquiescing to the Examiner's rejection, Applicants have amended claim 4 as recommended by the Examiner. Applicants respectfully request reconsideration and withdrawal of the foregoing 35 U.S.C 112, first paragraph rejection over claims 4, 7-12, 22, 31 and 35-39.

The Rejection of Claims 4, 7-12, 22, 31, under 35 U.S.C. §102(a), Should Be Withdrawn

Claims 4, 7-12, 22 and 31 are rejected under 35 U.S.C. §102(a) as being anticipated by Berlanga et al. (Eur. J. Biochem. 265:754-762 1999; EMBL accession numbers AJ243533 and AJ243428) and

Duesterhoeft et al. (EMBL accession numbers AL137627 and AL157497). Specifically, the Examiner states that the polynucleotide of Berlanga et al. and the polynucleotide of Duesterhoeft et al. "would hybridize under the highly stringent conditions recited in the claims to the polynucleotide of SEQ ID NO:1." The Examiner also adds that "Berlanga et al. also teaches the complete complement of the polynucleotide, host cells, vectors, and a method of producing the protein...the teachings of Berlanga et al. also anticipate claims 9-12 and 31". However, the Examiner notes "that the proposed amendment of claim 4 submitted by Applicants on 6/10/2003 and the cancellation of claim 35 may overcome the instant rejection."

In the interest of expediting prosecution, and without acquiescing to the Examiner's rejection, Applicants have amended claim 4 and cancelled claim 35 as recommended by the Examiner. Applicants respectfully request reconsideration and withdrawal of the foregoing 35 U.S.C 102(a) rejection over claims 4, 7-12, 22 and 31.

The Rejection of Claims 1-4, 7-8, 32-33, and 35-39 under 35 U.S.C. §102(e), Should Be Withdrawn

Claims 1-4, 7-8, 32-33 and 35-39 are provisionally rejected under 35 U.S.C. §102(e) as being "anticipated by copending Application No. 09/607,200, 09/644,867, 09/644,868, 09/644,869, 09/644,871, 09/649,161, 09/652,109, 09/710,280, 09/716,475, 09/726,175, 09/726,176, 09/726789 which have a common assignee (Millennium Pharmaceuticals Inc.) with the instant application. Based on the earlier effective U.S. filing date of the copending applications, they would constitute prior art under 35 U.S.C. 102(e), if published under 35 U.S.C. 122(b) or patented."

Applicants respectfully traverse this rejection. The sequences disclosed in Application No. 09/607,200, 09/644,867, 09/644,868, 09/644,869, 09/644,871, 09/649,161, 09/652,109, 09/710,280, 09/716,475, 09/726,175, 09/726,176 and 09/726789 do not anticipate the claimed invention because, as demonstrated below, the sequences disclosed in the prior applications do not fall within the scope of the presently pending claims.

Applicants have performed BLAST sequence alignments using the 5525 base pair nucleic acid sequence of SEQ ID NO:1 of the present invention and the polynucleotide sequences within each of the applications cited by the Examiner. Applicants provide herewith Exhibits A-K, wherein each exhibit corresponds to the best BLAST hit obtained for all of the sequences within each of the cited applications. As demonstrated by the sequence alignments provided in exhibits A-K, the longest sequence considered as a significant hit is merely 559 nucleotides long (see Exhibit G). Thus, the best hit obtained out of all of the cited applications, corresponds to only approximately 10% of the length of the nucleotide sequence of SEQ ID NO:1 of the present application. Additionally, Applicants note that BLASTs performed using the nucleotide sequence of SEQ ID NO:1 against the sequences of Application No. 09/652,109 cited by the Examiner, yielded no significant hits; hence, there is no corresponding exhibit for Application No.

09/652,109. Therefore, the sequences within the applications cited by the Examiner do not fall within the scope of the presently presented claims, and as such, are not prior art under 35 U.S.C. 102(e). Therefore, Applicants respectfully request reconsideration and withdrawal of the foregoing 35 U.S.C 102(e) rejection over claims 1-4, 7-8, 32-33 and 35-39.

CONCLUSIONS

In view of the amendments and remarks made herein, Applicants respectfully submit that the objections and rejections presented by the Examiner are now overcome and that this application is now in condition for allowance. Early notice to this effect is solicited.

If in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned.

It is believed this paper is being filed timely, as a request for a three-month extension of time is file concurrently herewith. In the event any additional extensions of time are necessary, the undersigned hereby authorizes the requisite fees to be charged to Deposit Account No. 501668.

Applicants submit herewith: 1) a request for a three-month extension of time; 2) an Associate Power of Attorney and 3) Exhibits A to K.
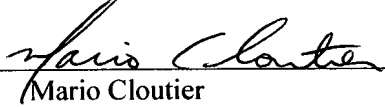
Entry of the remarks made herein is respectfully requested.

Respectfully submitted,

23 January 2004   MILLENNIUM PHARMACEUTICALS, INC.

By _____
Mario Cloutier
Limited Recognition under 37CFR §10.9
40 Landsdowne Street
Cambridge, MA 02139
Telephone - 617-577-3522
Facsimile - 617-551-8820

Exhibit A
(09/607,200 MPI1999-101P1R)

>39534625|johuh019h02t1|MPI1999-132P1|25 08 1999
>39534625|johuh019h02t1|MPI1999-103P1|29 06 1999
>39534625|johuh019h02t1|MPI1999-101P1R|Unknown
Length = 459

Plus Strand HSPs:

Score = 2220 (616.0 bits), Expect = 5.9e-176, P = 5.9e-176
Identities = 444/444 (100%), Positives = 444/444 (100%), Strand = Plus / Plus

```
Query:  1964 GGGCGAAGTGACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC 2023
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    16 GGGCGAAGTGACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC 75

Query:  2024 CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC 2083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    76 CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC 135

Query:  2084 CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA 2143
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   136 CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA 195

Query:  2144 CAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC 2203
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   196 CAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC 255

Query:  2204 GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA 2263
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   256 GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA 315

Query:  2264 GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCCTGCCTGCTTCAGA 2323
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   316 GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCCTGCCTGCTTCAGA 375

Query:  2324 TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA 2383
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   376 TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA 435

Query:  2384 TGAAGATTGCAATGAAAAGAATGG 2407
             ||||||||||||||||||||||||
Sbjct:   436 TGAAGATTGCAATGAAAAGAATGG 459
```

Exhibit B
(09/644,867 MPI1999-142P1R)

>43542170|jthza178f07t1|MPI1999-142P1|27 08 1999
>43542170|jthza178f07t1|MPI1999-142P1R|Unknown
Length = 433

Plus Strand HSPs:

Score = 1620 (450.2 bits), Expect = 4.2e-149, Sum P(2) = 4.2e-149
Identities = 324/324 (100%), Positives = 324/324 (100%), Strand = Plus / Plus

```
Query:   1860 GCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCTACGCAGTGAAG 1919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     35 GCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCTACGCAGTGAAG 94

Query:   1920 CGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAAGGGCGAAGTGACACTG 1979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     95 CGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAAGGGCGAAGTGACACTG 154

Query:   1980 CTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAGCGGCAC 2039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    155 CTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAGCGGCAC 214

Query:   2040 GAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCCCCTGGCCAAGGATGAC 2099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    215 GAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCCCCTGGCCAAGGATGAC 274

Query:   2100 CGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGACAGCGTAGAGGCCGCC 2159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    275 CGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGACAGCGTAGAGGCCGCC 334

Query:   2160 GCGCCGCCACCCATCCTCAGCAGC 2183
              ||||||||||||||||||||||||
Sbjct:    335 GCGCCGCCACCCATCCTCAGCAGC 358
```

Score = 340 (96.5 bits), Expect = 4.2e-149, Sum P(2) = 4.2e-149
Identities = 68/68 (100%), Positives = 68/68 (100%), Strand = Plus / Plus

```
Query:   2189 GGAGTGGAGCACTTCGGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGG 2248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    366 GGAGTGGAGCACTTCGGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGG 425

Query:   2249 CTCCAGCG 2256
              ||||||||
Sbjct:    426 CTCCAGCG 433
```

Exhibit C
(09/644,868 MPI1999-137P1R)

>11358048|jrhoc031d04t1|MPI1999-137P1|27 08 1999
>11358048|jrhoc031d04t1|MPI1999-137P1R|Unknown
Length = 507

Plus Strand HSPs:

Score = 2226 (617.7 bits), Expect = 8.1e-190, Sum P(2) = 8.1e-190
Identities = 446/447 (99%), Positives = 446/447 (99%), Strand = Plus / Plus

```
Query:   1854  AAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCTACGCA  1913
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:      1  AAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTGCTACGCA  60

Query:   1914  GTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAAGGGCGAAGTG  1973
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     61  GTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAAGGGCGAAGTG  120

Query:   1974  ACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAG  2033
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    121  ACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAG  180

Query:   2034  CGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCCCCTGGCCAAG  2093
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    181  CGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCCCCTGGCCAAG  240

Query:   2094  GATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGACAGCGTAGAG  2153
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    241  GATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGACAGCGTAGAG  300

Query:   2154  GCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTCGGGCGAGCGC  2213
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    301  GCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTCGGGCGAGCGC  360

Query:   2214  TCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGAGGACGACGAC  2273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    361  TCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGAGGACGACGAC  420

Query:   2274  GAGGACGAGCACGGTGGCGTCTTCTCC  2300
               |||||||||||||||||||||||| |||
Sbjct:    421  GAGGACGAGCACGGTGGCGTCTTTTCC  447
```

Score = 223 (64.2 bits), Expect = 8.1e-190, Sum P(2) = 8.1e-190
Identities = 47/50 (94%), Positives = 47/50 (94%), Strand = Plus / Plus

```
Query:   2296  TCTCCCAGTCCTTCCTGCCTGCTTCAGATTCTGAAAGTGATATTATCTTT  2345
               | | |||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct:    442  TTTTCCAGTCCTTCCTGCCTGCTTTAGATTCTGAAAGTGATATTATCTTT  491
```

Exhibit D
(09/644,869 MPI1999-151P1R)

```
>44440608|jThda113d02t1|MPI1999-151P1|27 08 1999
        >44440608|jThda113d02t1|MPI1999-151P1R|Unknown
        Length = 415


  Plus Strand HSPs:

 Score = 1052 (293.2 bits), Expect = 1.7e-156, Sum P(2) = 1.7e-156
 Identities = 216/226 (95%), Positives = 216/226 (95%), Strand = Plus / Plus

Query:   4589 GCAAAATCTGAAGGGGTCATTTTCTAATGCTTCAGGTTTGTTTGAAATCCATGGAGCAAC 4648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:      3 GCAAAATCTGAAGGGGTCATTTTCTAATGCTTCAGGTTTGTTTGAAATCCATGGAGCAAC 62

Query:   4649 AGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCG 4708
              || ||   |  |||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct:     63 AGGGGNNCNCATTGTGAGTGTGCTANCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCG 122

Query:   4709 CTATGAAACTCAGGTACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAG 4768
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct:    123 CTATGAAACTCAGGTNCAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAG 182

Query:   4769 CAGTGAAATTGAAATTCTGGCTGTGGATCTACCCAAAGAAACAATA 4814
              ||| ||||||||||||||||||||||||||||||||||| ||  |||
Sbjct:    183 CAGNGAAATTGAAATTCTGGCTGTGGATCTACCCAAAGCAAAGATA 228

 Score = 998 (278.3 bits), Expect = 1.7e-156, Sum P(2) = 1.7e-156
 Identities = 206/214 (96%), Positives = 206/214 (96%), Strand = Plus / Plus

Query:   4880 GCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACAT 4939
              |||||     |   |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    202 GCTGTGGATCTACCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACAT 261

Query:   4940 CAAAGTAGAAAAAAAGGTGTCTGTGCTATTTCTGTACAGCTATAGAGATGACTACTACAG 4999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    262 CAAAGTAGAAAAAAAGGTGTCTGTGCTATTTCTGTACAGCTATAGAGATGACTACTACAG 321

Query:   5000 AATCTTATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATA 5059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    322 AATCTTATTTTAACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATA 381

Query:   5060 CTGGAATAATGGAATGTTGTACATTCATCATAAT 5093
              ||||||||||||||||| ||||||||||||||||
Sbjct:    382 CTGGAATAATGGAATGGTGTACATTCATCATAAT 415
```

Exhibit E
(09/644,871 MPI1999-136PIR)

```
>33384347|jrhob212d08t1|MPI1999-136P1|27 08 1999
        >33384347|jrhob212d08t1|MPI1999-136P1R|Unknown
        Length = 462
```

Plus Strand HSPs:

Score = 1970 (546.9 bits), Expect = 2.2e-159, Sum P(2) = 2.2e-159
Identities = 396/400 (99%), Positives = 396/400 (99%), Strand = Plus / Plus

```
Query:  1109 ACTGGTAAAATTGAGCCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCA 1168
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    25 ACTGGTAAAATTGAGCCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCA 84

Query:  1169 AGACGACTCCATCGTGGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGC 1228
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    85 AGACGACTCCATCGTGGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGC 144

Query:  1229 ACACCTGAGCCACTCAGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCT 1288
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct:   145 ACACCTGAGCCACTCAGGCCCCATCCCTGTGCATCAGCTTCGNAGGTACACAGCTCAGCT 204

Query:  1289 CCTGTCAGGCCTTGATTATCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATC 1348
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   205 CCTGTCAGGCCTTGATTATCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATC 264

Query:  1349 TAATGTCTTGGTGGATGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCG 1408
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct:   265 TAATGTCTTGGTGGATGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTNTAAGCG 324

Query:  1409 CCTCGCAGACATTTGCAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAA 1468
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   325 CCTNGCAGACATTTGCAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAA 384

Query:  1469 TGCTCTGCCTTATAAAACGGGGAAGAAAGGAGATGTTTGG 1508
             |||||||||||||||||||||||||||||||||||||||| |
Sbjct:   385 TGCTCTGCCTTATAAAACGGGGAAGAAAGGAGATGTTTTG 424
```

Score = 113 (33.8 bits), Expect = 2.2e-159, Sum P(2) = 2.2e-159
Identities = 29/37 (78%), Positives = 29/37 (78%), Strand = Plus / Plus

```
Query:  1498 GAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCT 1534
             || | || | ||||||||||||    |||||||||||
Sbjct:   416 GATGTTTTGGCCGTCTTGGCCTTTCTCTGCTGTCCCT 452
```

>42245831|jThMc110e02t2|MPI1999-147P1|27 08 1999
>42245831|jThMc110e02t2|MPI1999-147P1R|Unknown
Length = 456

Plus Strand HSPs:

Score = 1311 (364.8 bits), Expect = 9.5e-169, Sum P(3) = 9.5e-169
Identities = 263/264 (99%), Positives = 263/264 (99%), Strand = Plus / Plus

```
Query:   3357 AACGAAGCTGCCCTATTCATGGACCACAGCGGGATGCTGGTGATGCTTCCTTTTGACCTG 3416
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    150 ACCGAAGCTGCCCTATTCATGGACCACAGCGGGATGCTGGTGATGCTTCCTTTTGACCTG 209

Query:   3417 CGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTTAAAACGATACTGC 3476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    210 CGGATCCCTTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTTAAAACGATACTGC 269

Query:   3477 ATAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAAAGAACTTCTGGAG 3536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    270 ATAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAAAGAACTTCTGGAG 329

Query:   3537 TGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCACTGCTGAAATTATC 3596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    330 TGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCACTGCTGAAATTATC 389

Query:   3597 TACACTATCTATGAAATCATCCAA 3620
              ||||||||||||||||||||||||
Sbjct:    390 TACACTATCTATGAAATCATCCAA 413
```

Score = 720 (201.5 bits), Expect = 9.5e-169, Sum P(3) = 9.5e-169
Identities = 144/144 (100%), Positives = 144/144 (100%), Strand = Plus / Plus

```
Query:   3216 CTGAAGGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATC 3275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:      8 CTGAAGGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATC 67

Query:   3276 ATCCGCATCTTTAAAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCCGA 3335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     68 ATCCGCATCTTTAAAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCCGA 127

Query:   3336 AACAGACAAATATATGAGCACAAC 3359
              ||||||||||||||||||||||||
Sbjct:    128 AACAGACAAATATATGAGCACAAC 151
```

Score = 221 (63.6 bits), Expect = 9.5e-169, Sum P(3) = 9.5e-169
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

```
Query:   3617 CCAAGAGTTTCCAGCACTTCAGGAAAGAAATTACAGTATTTATTTG 3662
              | |||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    411 CAAAGAGTTTCCAGCACTTCAGGAAAGAAATTACAGTATTTATTTG 456
```

```
>14993350|jthKa058c04t1|MBIO1999-104P1|.10 11 1999
        >14993350|jthKa058c04t1|MBIO1999-104P1R|Unknown
        Length = 549
```

Plus Strand HSPs:

```
Score = 2510 (696.1 bits), Expect = 1.7e-204, Sum P(2) = 1.7e-204
Identities = 502/502 (100%), Positives = 502/502 (100%), Strand = Plus / Plus

Query:  3507 GATCGATTTCATCCCAAAGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACC 3566
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    48 GATCGATTTCATCCCAAAGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACC 107

Query:  3567 AACAGCTTTCTGCCCACTGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTT 3626
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   108 AACAGCTTTCTGCCCACTGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTT 167

Query:  3627 CCAGCACTTCAGGAAAGAAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCA 3686
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   168 CCAGCACTTCAGGAAAGAAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCA 227

Query:  3687 ATACTCTTACACTGTGGGATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTAT 3746
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   228 ATACTCTTACACTGTGGGATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTAT 287

Query:  3747 GATGCTGTGACAGAGAAGCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCT 3806
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   288 GATGCTGTGACAGAGAAGCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCT 347

Query:  3807 TTGTCTTCTAATAGTCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAA 3866
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   348 TTGTCTTCTAATAGTCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAA 407

Query:  3867 GATCTTATGCCAACAATAAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTG 3926
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   408 GATCTTATGCCAACAATAAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTG 467

Query:  3927 AAGTATGGCTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAG 3986
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   468 AAGTATGGCTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAG 527

Query:  3987 TTACAGGTCTTGATCAATTTGG 4008
             ||||||||||||||||||||||
Sbjct:   528 TTACAGGTCTTGATCAATTTGG 549

Score = 115 (34.3 bits), Expect = 1.7e-204, Sum P(2) = 1.7e-204
Identities = 23/23 (100%), Positives = 23/23 (100%), Strand = Plus / Plus

Query:  3484 GTGTGTTCAGGCCGCGCAAGTTA 3506
             |||||||||||||||||||||||
Sbjct:    24 GTGTGTTCAGGCCGCGCAAGTTA 46
```

>57228667|johvb399h05t1|MPI1999-263P1|19 11 1999
>57228667|johvb399h05t1|MPI1999-263P1R|Unknown
Length = 559

Plus Strand HSPs:

Score = 855 (238.8 bits), Expect = 6.6e-160, Sum P(6) = 6.6e-160
Identities = 183/198 (92%), Positives = 183/198 (92%), Strand = Plus / Plus

```
Query:  5053 GCTTATACTGGAATAATGGAATGTTGTACATTCATCATAATTTAAAATTAAATTCTAAGA 5112
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   188 GCTTATACTGGAATAATGGAATGTTGTACATTCATCATAATTTAAAATTAAATTCTAAGA 247

Query:  5113 AGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAGGA 5172
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   248 AGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAGCACTTTGGGAAGCCAAGGCAGGA 307

Query:  5173 AGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAGACCCCATCTCT 5232
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct:   308 AGACTGCTTGAAACCAGGAGTTTGAGACCAGCCTGAGCAACAAAGCAAGGACCCCATCTC 367

Query:  5233 ATAAAAACTAAAAAAATT 5250
             ||||    ||||||| |
Sbjct:   368 TATAAAAACTAAAAAAAT 385
```

Score = 617 (173.0 bits), Expect = 6.6e-160, Sum P(6) = 6.6e-160
Identities = 125/127 (98%), Positives = 125/127 (98%), Strand = Plus / Plus

```
Query:  4907 CCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGTGCT 4966
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    44 CCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGTGCT 103

Query:  4967 ATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAACTGT 5026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   104 ATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAACTGT 163

Query:  5027 CGTTAAC 5033
             ||| | |
Sbjct:   164 CGTAACC 170
```

Score = 491 (138.2 bits), Expect = 6.6e-160, Sum P(6) = 6.6e-160
Identities = 99/100 (99%), Positives = 99/100 (99%), Strand = Plus / Plus

```
Query:  5219 AAGACCCCATCTCTATAAAAACTAAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTAG 5278
             | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   355 AGGACCCCATCTCTATAAAAACTAAAAAAATTAGTTGGGCATGGTGGCACATGCCTGTAG 414

Query:  5279 TCCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCT 5318
             ||||||||||||||||||||||||||||||||||||||||
Sbjct:   415 TCCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCT 454
```

Score = 255 (73.0 bits), Expect = 6.6e-160, Sum P(6) = 6.6e-160
Identities = 73/101 (72%), Positives = 73/101 (72%), Strand = Plus / Plus

```
Query:  5316 CCTCAGGAGGTTGAGGCTGCAGTGAGCTGTGACTGCGCCACTGCACTCCAGTCTGGGACA 5375
             | |||||||||||||||||||||||||||||||||||||| |        || |||||||||
Sbjct:   453 CTTCAGGAGGTTGAGGCTGCAGTGAGCTGTGACTGCCCACTGNACTTCAAGTCTGGGACA 512

Query:  5376 ACAGAGCAAGACCCTGTCTTAAAAAAAAAAAGAAAAAAAA 5416
             | ||||||      | |||||||||||    |||||||
Sbjct:   513 CAGAGCAAGGACCCCTGTCTTAAAAAAAAAAAGGAAAAAA 553
```

Score = 141 (41.5 bits), Expect = 1.5e-150, Sum P(6) = 1.5e-150

Exhibit H
(09/716,475 MPI1999-263PIR)

```
Identities = 29/30 (96%), Positives = 29/30 (96%), Strand = Plus / Plus

Query:  5387 CCCTGTCTTAAAAAAAAAAAGAAAAAAAA 5416
             |||||||||||||||||||||| ||||||||
Sbjct:   525 CCCTGTCTTAAAAAAAAAAAGGAAAAAAA 554

 Score = 115 (34.3 bits), Expect = 6.6e-160, Sum P(6) = 6.6e-160
 Identities = 23/23 (100%), Positives = 23/23 (100%), Strand = Plus / Plus

Query:  5030 TAACCTCATTCAAACAGACAGAG 5052
             |||||||||||||||||||||||
Sbjct:   166 TAACCTCATTCAAACAGACAGAG 188

 Score = 96 (29.1 bits), Expect = 6.6e-160, Sum P(6) = 6.6e-160
 Identities = 20/21 (95%), Positives = 20/21 (95%), Strand = Plus / Plus

Query:  4887 CGCCTGCCAAAGCAAAGATAC 4907
             ||||||||||||||||||| |
Sbjct:    25 CGCCTGCCAAAGCAAAGATCC 45
```

Exhibit I
(09/726,175 MPI1999-252P1R)

>49723077|jThYa179b12t1|MPI1999-252P1|29 11 1999
>49723077|jThYa179b12t1|MPI1999-252P1R|Unknown
Length = 390

Plus Strand HSPs:

Score = 1846 (512.7 bits), Expect = 9.4e-145, P = 9.4e-145
Identities = 370/371 (99%), Positives = 370/371 (99%), Strand = Plus / Plus

```
Query:  2653 TAGGTGATTTTGGTTTGGCGACAGACCATCTAGCCTTTTCTGCTGACAGCAAACAAGACG 2712
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    20 TTGGTGATTTTGGTTTGGCGACAGACCATCTAGCCTTTTCTGCTGACAGCAAACAAGACG 79

Query:  2713 ATCAGACAGGAGACTTGATTAAGTCAGACCCTTCAGGTCACTTAACTGGGATGGTTGGCA 2772
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    80 ATCAGACAGGAGACTTGATTAAGTCAGACCCTTCAGGTCACTTAACTGGGATGGTTGGCA 139

Query:  2773 CTGCTCTCTATGTAAGCCCAGAGGTCCAAGGAAGCACCAAATCTGCATACAACCAGAAAG 2832
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   140 CTGCTCTCTATGTAAGCCCAGAGGTCCAAGGAAGCACCAAATCTGCATACAACCAGAAAG 199

Query:  2833 TGGATCTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCCTATCACCCCATGGTCACGG 2892
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   200 TGGATCTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCCTATCACCCCATGGTCACGG 259

Query:  2893 CTTCAGAAAGGATCTTTGTTCTCAACCAACTCAGAGATCCCACTTCGCCTAAGTTTCCAG 2952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   260 CTTCAGAAAGGATCTTTGTTCTCAACCAACTCAGAGATCCCACTTCGCCTAAGTTTCCAG 319

Query:  2953 AAGACTTTGACGATGGAGAGCATGCAAAGCAGAAATCAGTCATCTCCTGGCTGTTGAACC 3012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   320 AAGACTTTGACGATGGAGAGCATGCAAAGCAGAAATCAGTCATCTCCTGGCTGTTGAACC 379

Query:  3013 ACGATCCAGCA 3023
             |||||||||||
Sbjct:   380 ACGATCCAGCA 390
```

Exhibit J
(09/726,126 MBIO1999-120P1R)

```
>42130623|jthYa061g01t1|MBIO1999-120P1|29 11 1999
        >42130623|jthYa061g01t1|MBIO1999-120P1R|Unknown
        Length = 393

  Plus Strand HSPs:

  Score = 1868 (518.7 bits), Expect = 1.4e-146, P = 1.4e-146
  Identities = 374/375 (99%), Positives = 374/375 (99%), Strand = Plus / Plus

Query:  3635 TCAGGAAAGAAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTT 3694
             |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    19 TNAGGAAAGAAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTT 78

Query:  3695 ACACTGTGGGATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGT 3754
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    79 ACACTGTGGGATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGT 138

Query:  3755 GACAGAGAAGCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTC 3814
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   139 GACAGAGAAGCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTC 198

Query:  3815 TAATAGTCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTAT 3874
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   199 TAATAGTCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTAT 258

Query:  3875 GCCAACAATAAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGG 3934
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   259 GCCAACAATAAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGG 318

Query:  3935 CTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTTACAGGT 3994
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   319 CTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTTACAGGT 378

Query:  3995 CTTGATCAATTTGGG 4009
             |||||||||||||||
Sbjct:   379 CTTGATCAATTTGGG 393
```

```
>48772799|jlhxc096f07t1|MPI1999-210P1|30 11 1999
         >48772799|jlhxc096f07t1|MPI1999-210P1R|Unknown
         Length = 304
```

Plus Strand HSPs:

Score = 1045 (291.3 bits), Expect = 1.7e-100, Sum P(3) = 1.7e-100
Identities = 225/250 (90%), Positives = 225/250 (90%), Strand = Plus / Plus

```
Query:    69 GGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGAGCCTCCGGAGAGCTACCCGCAACGA 128
             |||| | | ||| |||| |      | | |   ||||||||||||||||| ||||| ||||
Sbjct:    55 GGGGCCGGGGGGCCCCCGGCCGCGGNCGGTACCGAGCCTCCGGAGAGCNACCCGGAACGN 114

Query:   129 CAGGACCACGAGCTACAGGCCCTGGAGGCCATCTACGGCGCGGACTTCCAAGACCTGCGG 188
             |||||||||| |||||||||||||||||||||||||||||| |||||||| || ||||||||
Sbjct:   115 CAGGACCACNAGCTACAGGCCCTGGAGGCCATCTACGGCNCGGACTTNCANNACCTGCGG 174

Query:   189 CCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGAAATCAATTTAGTTTTGTACCCTCAA 248
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   175 CCGGACGCTTGNGGACCGGTCAAAGAGCCCCCTGAAATCAATTTAGTTTTGTACCCTCAA 234

Query:   249 GGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGAGGGTTAAATGCCCACCTACC 308
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct:   235 GGCCTAACTGGTGAAGAAGTATATGTNAAAGTGGATTTGAGGGTTAAATGCCCACCTACC 294

Query:   309 TATCCAGATG 318
             ||||||||||
Sbjct:   295 TATCCAGATG 304
```

Score = 302 (86.0 bits), Expect = 1.7e-100, Sum P(3) = 1.7e-100
Identities = 64/70 (91%), Positives = 64/70 (91%), Strand = Plus / Plus

```
Query:    32 AAGGCCGCCCTGCCTTGGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCG 91
             ||||||| |||||||||||||| ||||||||||||||||||||| ||||||||||| ||
Sbjct:    17 AAGGCCGNCCTGCCTTGGGCGCANCGCTGCCATGGCTGGGGGCCGGGGGGGCCCCCGGCCG 76

Query:    92 CGGCCGGGAC 101
             ||| ||| ||
Sbjct:    77 CGGNCGGTAC 86
```

Score = 82 (25.2 bits), Expect = 1.7e-100, Sum P(3) = 1.7e-100
Identities = 18/20 (90%), Positives = 18/20 (90%), Strand = Plus / Plus

```
Query:    18 ACCGCCGCCCAGGCAAGGCC 37
             ||||||||||||||| | |
Sbjct:     2 ACCGCCGCCCAGGCAAAGGC 21
```